



SEQUENCE LISTING

<110> Beamer, Less
Eisenberg, David
Carroll, Stephen F.

<120> BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN:
CRYSTALLIZATION, X-RAY DIFFRACTION, THREE-DIMENSIONAL
STRUCTURE DETERMINATION, RATIONAL DRUG DESIGN AND
MOLECULAR MODELING OF RELATED PROTEINS

<130> 11034US02

<140> 09/446,415

<141> 2000-07-19

<150> 08/879,565

<151> 1997-06-20

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

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<223> "rBPI"

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Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile
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Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile
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Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu
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cag aag gag ctg aag agg atc aag att cct gac tac tca gac agc ttt 246
Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe
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aag atc aag cat ctt ggg aag ggg cat tat agc ttc tac agc atg gac	294
Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp	
45 50 55	
atc cgt gaa ttc cag ctt ccc agt tcc cag ata agc atg gtg ccc aat	342
Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn	
60 65 70	
gtg ggc ctt aag ttc tcc atc agc aac gcc aat atc aag atc agc ggg	390
Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly	
75 80 85	
aaa tgg aag gca caa aag aga ttc tta aaa atg agc ggc aat ttt gac	438
Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp	
90 95 100 105	
ctg agc ata gaa ggc atg tcc att tcg gct gat ctg aag ctg ggc agt	486
Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser	
110 115 120	
aac ccc acg tca ggc aag ccc acc atc acc tgc tcc agc tgc agc agc	534
Asn Pro Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser Ser	
125 130 135	
cac atc aac agt gtc cac gtg cac atc tca aag agc aaa gtc ggg tgg	582
His Ile Asn Ser Val His Val His Ile Ser Lys Ser Lys Val Gly Trp	
140 145 150	
ctg atc caa ctc ttc cac aaa aaa att gag tct gcg ctt cga aac aag	630
Leu Ile Gln Leu Phe His Lys Lys Ile Glu Ser Ala Leu Arg Asn Lys	
155 160 165	
atg aac agc cag gtc tgc gag aaa gtg acc aat tct gta tcc tcc aag	678
Met Asn Ser Gln Val Cys Glu Lys Val Thr Asn Ser Val Ser Ser Lys	
170 175 180 185	
ctg caa cct tat ttc cag act ctg cca gta atg acc aaa ata gat tct	726
Leu Gln Pro Tyr Phe Gln Thr Leu Pro Val Met Thr Lys Ile Asp Ser	
190 195 200	
gtg gct gga atc aac tat ggt ctg gtg gca cct cca gca acc acg gct	774
Val Ala Gly Ile Asn Tyr Gly Leu Val Ala Pro Pro Ala Thr Thr Ala	
205 210 215	
gag acc ctg gat gta cag atg aag ggg gag ttt tac agt gag aac cac	822
Glu Thr Leu Asp Val Gln Met Lys Gly Glu Phe Tyr Ser Glu Asn His	
220 225 230	
cac aat cca cct ccc ttt gct cca cca gtg atg gag ttt ccc gct gcc	870
His Asn Pro Pro Pro Phe Ala Pro Pro Val Met Glu Phe Pro Ala Ala	
235 240 245	
cat gac cgc atg gta tac ctg ggc ctc tca gac tac ttc ttc aac aca	918
His Asp Arg Met Val Tyr Leu Gly Leu Ser Asp Tyr Phe Phe Asn Thr	
250 255 260 265	
gcc ggg ctt gta tac caa gag gct ggg gtc ttg aag atg acc ctt aga	966
Ala Gly Leu Val Tyr Gln Glu Ala Gly Val Leu Lys Met Thr Leu Arg	
270 275 280	

gat gac atg att cca aag gag tcc aaa ttt cga ctg aca acc aag ttc	1014
Asp Asp Met Ile Pro Lys Glu Ser Lys Phe Arg Leu Thr Thr Lys Phe	
285 290 295	
ttt gga acc ttc cta cct gag gtg gcc aag aag ttt ccc aac atg aag	1062
Phe Gly Thr Phe Leu Pro Glu Val Ala Lys Lys Phe Pro Asn Met Lys	
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ata cag atc cat gtc tca gcc tcc acc ccg cca cac ctg tct gtg cag	1110
Ile Gln Ile His Val Ser Ala Ser Thr Pro Pro His Leu Ser Val Gln	
315 320 325	
ccc acc ggc ctt acc ttc tac cct gcc gtg gat gtc cag gcc ttt gcc	1158
Pro Thr Gly Leu Thr Phe Tyr Pro Ala Val Asp Val Gln Ala Phe Ala	
330 335 340 345	
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Val Leu Pro Asn Ser Ser Leu Ala Ser Leu Phe Leu Ile Gly Met His	
350 355 360	
aca act ggt tcc atg gag gtc agc gcc gag tcc aac agg ctt gtt gga	1254
Thr Thr Gly Ser Met Glu Val Ser Ala Glu Ser Asn Arg Leu Val Gly	
365 370 375	
gag ctc aag ctg gat agg ctg ctc ctg gaa ctg aag cac tca aat att	1302
Glu Leu Lys Leu Asp Arg Leu Leu Leu Glu Leu Lys His Ser Asn Ile	
380 385 390	
ggc ccc ttc ccg gtt gaa ttg ctg cag gat atc atg aac tac att gta	1350
Gly Pro Phe Pro Val Glu Leu Leu Gln Asp Ile Met Asn Tyr Ile Val	
395 400 405	
ccc att ctt gtg ctg ccc agg gtt aac gag aaa cta cag aaa ggc ttc	1398
Pro Ile Leu Val Leu Pro Arg Val Asn Glu Lys Leu Gln Lys Gly Phe	
410 415 420 425	
cct ctc ccg acg ccg gcc aga gtc cag ctc tac aac gta gtg ctt cag	1446
Pro Leu Pro Thr Pro Ala Arg Val Gln Leu Tyr Asn Val Val Leu Gln	
430 435 440	
cct cac cag aac ttc ctg ctg ttc ggt gca gac gtt gtc tat aaa	1491
Pro His Gln Asn Phe Leu Leu Phe Gly Ala Asp Val Val Tyr Lys	
445 450 455	
tgaaggcacc aggggtgccg ggggctgtca gccgcacctg ttcttgatgg gctgtggggc	1551
accggctgcc tttccccagg gaatcctctc cagatcttaa ccaagagccc cttgcaaact	1611
tcttcgactc agattcagaa atgatctaaa cacgaggaaa cattattcat tggaaaagtg	1671
catgggtgtgt attttaggga ttatgagctt ctttcaaggg ctaaggctgc agagatatatt	1731
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<223> "rBPI"

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Asn	Pro	Gly	Val	Val	Val	Arg	Ile	Ser	Gln	Lys	Gly	Leu	Asp	Tyr	Ala	5	10	15		
Ser	Gln	Gln	Gly	Thr	Ala	Ala	Leu	Gln	Lys	Glu	Leu	Lys	Arg	Ile	Lys	20	25	30		
Ile	Pro	Asp	Tyr	Ser	Asp	Ser	Phe	Lys	Ile	Lys	His	Leu	Gly	Lys	Gly	35	40	45		
His	Tyr	Ser	Phe	Tyr	Ser	Met	Asp	Ile	Arg	Glu	Phe	Gln	Leu	Pro	Ser	50	55	60	65	
Ser	Gln	Ile	Ser	Met	Val	Pro	Asn	Val	Gly	Leu	Lys	Phe	Ser	Ile	Ser	70	75	80		
Asn	Ala	Asn	Ile	Lys	Ile	Ser	Gly	Lys	Trp	Lys	Ala	Gln	Lys	Arg	Phe	85	90	95		
Leu	Lys	Met	Ser	Gly	Asn	Phe	Asp	Leu	Ser	Ile	Glu	Gly	Met	Ser	Ile	100	105	110		
Ser	Ala	Asp	Leu	Lys	Leu	Gly	Ser	Asn	Pro	Thr	Ser	Gly	Lys	Pro	Thr	115	120	125		
Ile	Thr	Cys	Ser	Ser	Cys	Ser	Ser	His	Ile	Asn	Ser	Val	His	Val	His	130	135	140	145	
Ile	Ser	Lys	Ser	Lys	Val	Gly	Trp	Leu	Ile	Gln	Leu	Phe	His	Lys	Lys	150	155	160		
Ile	Glu	Ser	Ala	Leu	Arg	Asn	Lys	Met	Asn	Ser	Gln	Val	Cys	Glu	Lys	165	170	175		
Val	Thr	Asn	Ser	Val	Ser	Ser	Lys	Leu	Gln	Pro	Tyr	Phe	Gln	Thr	Leu	180	185	190		
Pro	Val	Met	Thr	Lys	Ile	Asp	Ser	Val	Ala	Gly	Ile	Asn	Tyr	Gly	Leu	195	200	205		
Val	Ala	Pro	Pro	Ala	Thr	Thr	Ala	Glu	Thr	Leu	Asp	Val	Gln	Met	Lys	210	215	220	225	
Gly	Glu	Phe	Tyr	Ser	Glu	Asn	His	His	Asn	Pro	Pro	Pro	Phe	Ala	Pro	230	235	240		
Pro	Val	Met	Glu	Phe	Pro	Ala	Ala	His	Asp	Arg	Met	Val	Tyr	Leu	Gly	245	250	255		
Leu	Ser	Asp	Tyr	Phe	Phe	Asn	Thr	Ala	Gly	Leu	Val	Tyr	Gln	Glu	Ala	260	265	270		

Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser
 275 280 285

Lys Phe Arg Leu Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu Val
 290 295 300 305

Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser
 310 315 320

Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro
 325 330 335

Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala
 340 345 350

Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser
 355 360 365

Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu
 370 375 380 385

Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu
 390 395 400

Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val
 405 410 415

Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val
 420 425 430

Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe
 435 440 445

Gly Ala Asp Val Val Tyr Lys
 450 455

<210> 3
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<220>
 <223> bactericidal/permeability-increasing protein (BPI)
 (Figure 5)

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 1 5 10 15

Ala Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile
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Lys Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys
 35 40 45

Gly His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro
 50 55 60

Ser	Ser	Gln	Ile	Ser	Met	Val	Pro	Asn	Val	Gly	Leu	Lys	Phe	Ser	Ile	65	70	75	80
Ser	Asn	Ala	Asn	Ile	Lys	Ile	Ser	Gly	Lys	Trp	Lys	Ala	Gln	Lys	Arg	85	90	95	
Phe	Leu	Lys	Met	Ser	Gly	Asn	Phe	Asp	Leu	Ser	Ile	Glu	Gly	Met	Ser	100	105	110	
Ile	Ser	Ala	Asp	Leu	Lys	Leu	Gly	Ser	Asn	Pro	Thr	Ser	Gly	Lys	Pro	115	120	125	
Thr	Ile	Thr	Cys	Ser	Ser	Cys	Ser	Ser	His	Ile	Asn	Ser	Val	His	Val	130	135	140	
His	Ile	Ser	Lys	Ser	Lys	Val	Gly	Trp	Leu	Ile	Gln	Leu	Phe	His	Lys	145	150	155	160
Lys	Ile	Glu	Ser	Ala	Leu	Arg	Asn	Lys	Met	Asn	Ser	Gln	Val	Cys	Glu	165	170	175	
Lys	Val	Thr	Asn	Ser	Val	Ser	Ser	Glu	Leu	Gln	Pro	Tyr	Phe	Gln	Thr	180	185	190	
Leu	Pro	Val	Met	Thr	Lys	Ile	Asp	Ser	Val	Ala	Gly	Ile	Asn	Tyr	Gly	195	200	205	
Leu	Val	Ala	Pro	Pro	Ala	Thr	Thr	Ala	Glu	Thr	Leu	Asp	Val	Gln	Met	210	215	220	
Lys	Gly	Glu	Phe	Tyr	Ser	Glu	Asn	His	His	Asn	Pro	Pro	Pro	Phe	Ala	225	230	235	240
Pro	Pro	Val	Met	Glu	Phe	Pro	Ala	Ala	His	Asp	Arg	Met	Val	Tyr	Leu	245	250	255	
Gly	Leu	Ser	Asp	Tyr	Phe	Phe	Asn	Thr	Ala	Gly	Leu	Val	Tyr	Gln	Glu	260	265	270	
Ala	Gly	Val	Leu	Lys	Met	Thr	Leu	Arg	Asp	Asp	Met	Ile	Pro	Lys	Glu	275	280	285	
Ser	Lys	Phe	Arg	Leu	Thr	Thr	Lys	Phe	Phe	Gly	Thr	Phe	Leu	Pro	Glu	290	295	300	
Val	Ala	Lys	Lys	Phe	Pro	Asn	Met	Lys	Ile	Gln	Ile	His	Val	Ser	Ala	305	310	315	320
Ser	Thr	Pro	Pro	His	Leu	Ser	Val	Gln	Pro	Thr	Gly	Leu	Thr	Phe	Tyr	325	330	335	
Pro	Ala	Val	Asp	Val	Gln	Ala	Phe	Ala	Val	Leu	Pro	Asn	Ser	Ser	Leu	340	345	350	
Ala	Ser	Leu	Phe	Leu	Ile	Gly	Met	His	Thr	Thr	Gly	Ser	Met	Glu	Val	355	360	365	
Ser	Ala	Glu	Ser	Asn	Arg	Leu	Val	Gly	Glu	Leu	Lys	Leu	Asp	Arg	Leu	370	375	380	

Leu Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu
 385 390 395 400

Leu Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg
 405 410 415

Val Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg
 420 425 430

Val Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu
 435 440 445

Phe Gly Ala Asp Val Val Tyr Lys
 450 455

<210> 4
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<220>
 <223> lipopolysaccharide binding protein (LBP) (Figure
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Ala Ala Gln Glu Gly Leu Leu Ala Leu Gln Ser Glu Leu Leu Arg Ile
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Thr Leu Pro Asp Phe Thr Gly Asp Leu Arg Ile Pro His Val Gly Arg
 35 40 45

Gly Arg Tyr Glu Phe His Ser Leu Asn Ile His Ser Cys Glu Leu Leu
 50 55 60

His Ser Ala Leu Arg Pro Val Pro Gly Gln Gly Leu Ser Leu Ser Ile
 65 70 75 80

Ser Asp Ser Ser Ile Arg Val Gln Gly Arg Trp Lys Val Arg Lys Ser
 85 90 95

Phe Phe Lys Leu Gln Gly Ser Phe Asp Val Ser Val Lys Gly Ile Ser
 100 105 110

Ile Ser Val Asn Leu Leu Leu Gly Ser Glu Ser Ser Gly Arg Pro Thr
 115 120 125

Val Thr Ala Ser Ser Cys Ser Ser Asp Ile Ala Asp Val Glu Val Asp
 130 135 140

Met Ser Gly Asp Leu Gly Trp Leu Leu Asn Leu Phe His Asn Gln Ile
 145 150 155 160

Glu Ser Lys Phe Gln Lys Val Leu Glu Ser Arg Ile Cys Glu Met Ile
 165 170 175

Gln Lys Ser Val Ser Ser Asp Leu Gln Pro Tyr Leu Gln Thr Leu Pro
 180 185 190

Val	Thr	Thr	Glu	Ile	Asp	Ser	Phe	Ala	Asp	Ile	Asp	Tyr	Ser	Leu	Val	195	200	205	
Glu	Ala	Pro	Arg	Ala	Thr	Ala	Gln	Met	Leu	Glu	Val	Met	Phe	Lys	Gly	210	215	220	
Glu	Ile	Phe	His	Arg	Asn	His	Arg	Ser	Pro	Val	Thr	Leu	Leu	Ala	Ala	225	230	235	240
Val	Met	Ser	Leu	Pro	Glu	Glu	His	Asn	Lys	Met	Val	Tyr	Phe	Ala	Ile	245	250	255	
Ser	Asp	Tyr	Val	Phe	Asn	Thr	Ala	Ser	Leu	Val	Tyr	His	Glu	Glu	Gly	260	265	270	
Tyr	Leu	Asn	Phe	Ser	Ile	Thr	Asp	Asp	Met	Ile	Pro	Pro	Asp	Ser	Asn	275	280	285	
Ile	Arg	Leu	Thr	Thr	Lys	Ser	Phe	Arg	Pro	Phe	Val	Pro	Arg	Leu	Ala	290	295	300	
Arg	Leu	Tyr	Pro	Asn	Met	Asn	Leu	Glu	Leu	Gln	Gly	Ser	Val	Pro	Ser	305	310	315	320
Ala	Pro	Leu	Leu	Asn	Phe	Ser	Pro	Gly	Asn	Leu	Ser	Val	Asp	Pro	Tyr	325	330	335	
Met	Glu	Ile	Asp	Ala	Phe	Val	Leu	Leu	Pro	Ser	Ser	Ser	Lys	Glu	Pro	340	345	350	
Val	Phe	Arg	Leu	Ser	Val	Ala	Thr	Asn	Val	Ser	Ala	Thr	Leu	Thr	Phe	355	360	365	
Asn	Thr	Ser	Lys	Ile	Thr	Gly	Phe	Leu	Lys	Pro	Gly	Lys	Val	Lys	Val	370	375	380	
Glu	Leu	Lys	Glu	Ser	Lys	Val	Gly	Leu	Phe	Asn	Ala	Glu	Leu	Leu	Glu	385	390	395	400
Ala	Leu	Leu	Asn	Tyr	Tyr	Ile	Leu	Asn	Thr	Phe	Tyr	Pro	Lys	Phe	Asn	405	410	415	
Asp	Lys	Leu	Ala	Glu	Gly	Phe	Pro	Leu	Pro	Leu	Leu	Lys	Arg	Val	Gln	420	425	430	
Leu	Tyr	Asp	Leu	Gly	Leu	Gln	Ile	His	Lys	Asp	Phe	Leu	Phe	Leu	Gly	435	440	445	
Ala	Asn	Val	Gln	Tyr	Met	Arg	Val									450	455		

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<211> 476

<212> PRT

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<223> phospholipid transfer protein (PLTP) (Figure 5)

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Val	Lys	Gln	Glu	Gly	Leu	Arg	Phe	Leu	Glu	Gln	Glu	Leu	Glu	Thr	Ile	20	25	30	
Thr	Ile	Pro	Asp	Leu	Arg	Gly	Lys	Glu	Gly	His	Phe	Tyr	Tyr	Asn	Ile	35	40	45	
Ser	Glu	Val	Lys	Val	Thr	Glu	Leu	Gln	Leu	Thr	Ser	Ser	Glu	Leu	Asp	50	55	60	
Phe	Gln	Pro	Gln	Gln	Glu	Leu	Met	Leu	Gln	Ile	Thr	Asn	Ala	Ser	Leu	65	70	75	
Gly	Leu	Arg	Phe	Arg	Arg	Gln	Leu	Leu	Tyr	Trp	Phe	Phe	Tyr	Asp	Gly	85	90	95	
Gly	Tyr	Ile	Asn	Ala	Ser	Ala	Glu	Gly	Val	Ser	Ile	Arg	Thr	Gly	Leu	100	105	110	
Glu	Leu	Ser	Arg	Asp	Pro	Ala	Gly	Arg	Met	Lys	Val	Ser	Asn	Val	Ser	115	120	125	
Cys	Gln	Ala	Ser	Val	Ser	Arg	Met	His	Ala	Ala	Phe	Gly	Gly	Thr	Phe	130	135	140	
Lys	Lys	Val	Tyr	Asp	Phe	Leu	Ser	Thr	Phe	Ile	Thr	Ser	Gly	Met	Arg	145	150	155	
Phe	Leu	Leu	Asn	Gln	Gln	Ile	Cys	Pro	Val	Leu	Tyr	His	Ala	Gly	Thr	165	170	175	
Val	Leu	Leu	Asn	Ser	Leu	Leu	Asp	Thr	Val	Pro	Val	Arg	Ser	Ser	Val	180	185	190	
Asp	Glu	Leu	Val	Gly	Ile	Asp	Tyr	Ser	Leu	Met	Lys	Asp	Pro	Val	Ala	195	200	205	
Ser	Thr	Ser	Asn	Leu	Asp	Met	Asp	Phe	Arg	Gly	Ala	Phe	Phe	Pro	Leu	210	215	220	
Thr	Glu	Arg	Asn	Trp	Ser	Leu	Pro	Asn	Arg	Ala	Val	Glu	Pro	Gln	Leu	225	230	235	
Gln	Glu	Glu	Glu	Arg	Met	Val	Tyr	Val	Ala	Phe	Ser	Glu	Phe	Phe	Phe	245	250	255	
Asp	Ser	Ala	Met	Glu	Ser	Tyr	Phe	Arg	Ala	Gly	Ala	Leu	Gln	Leu	Leu	260	265	270	
Leu	Val	Gly	Asp	Lys	Val	Pro	His	Asp	Leu	Asp	Met	Leu	Leu	Arg	Ala	275	280	285	
Thr	Tyr	Phe	Gly	Ser	Ile	Val	Leu	Leu	Ser	Pro	Ala	Val	Ile	Asp	Ser	290	295	300	
Pro	Leu	Lys	Leu	Glu	Leu	Arg	Val	Leu	Ala	Pro	Pro	Arg	Cys	Thr	Ile	305	310	315	

Lys Pro Ser Gly Thr Thr Ile Ser Val Thr Ala Ser Val Thr Ile Ala
325 330 335

Leu Val Pro Pro Asp Gln Pro Glu Val Gln Leu Ser Ser Met Thr Met
340 345 350

Asp Ala Arg Leu Ser Ala Lys Met Ala Leu Arg Gly Lys Ala Leu Arg
355 360 365

Thr Gln Leu Asp Leu Arg Arg Phe Arg Ile Tyr Ser Asn His Ser Ala
370 375 380

Leu Glu Ser Leu Ala Leu Ile Pro Leu Gln Ala Pro Leu Lys Thr Met
385 390 395 400

Leu Gln Ile Gly Val Met Pro Met Leu Asn Glu Arg Thr Trp Arg Gly
405 410 415

Val Gln Ile Pro Leu Pro Glu Gly Ile Asn Phe Val His Glu Val Val
420 425 430

Thr Asn His Ala Gly Phe Leu Thr Ile Gly Ala Asp Leu His Phe Ala
435 440 445

Lys Gly Leu Arg Glu Val Ile Glu Lys Asn Arg Pro Ala Asp Val Arg
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Ala Ser Thr Ala Pro Thr Pro Ser Thr Ala Ala Val
465 470 475

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5)

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20 25 30

Ser Tyr Pro Asp Ile Thr Gly Glu Lys Ala Met Met Leu Leu Gly Gln
35 40 45

Val Lys Tyr Gly Leu His Asn Ile Gln Ile Ser His Leu Ser Ile Ala
50 55 60

Ser Ser Gln Val Glu Leu Val Glu Ala Lys Ser Ile Asp Val Ser Ile
65 70 75 80

Gln Asn Val Ser Val Val Phe Lys Gly Thr Leu Lys Tyr Gly Tyr Thr
85 90 95

Thr Ala Trp Trp Leu Gly Ile Asp Gln Ser Ile Asp Phe Glu Ile Asp
100 105 110

Ser	Ala	Ile	Asp	Leu	Gln	Ile	Asn	Thr	Gln	Leu	Thr	Cys	Asp	Ser	Gly	115	120	125
Arg	Val	Arg	Thr	Asp	Ala	Pro	Asp	Cys	Tyr	Leu	Ser	Phe	His	Lys	Leu	130	135	140
Leu	Leu	His	Leu	Gln	Gly	Glu	Arg	Glu	Pro	Gly	Trp	Ile	Lys	Gln	Leu	145	150	155
Phe	Thr	Asn	Phe	Ile	Ser	Phe	Thr	Leu	Lys	Leu	Val	Leu	Lys	Gly	Gln	165	170	175
Ile	Cys	Lys	Glu	Ile	Asn	Val	Ile	Ser	Asn	Ile	Met	Ala	Asp	Phe	Val	180	185	190
Gln	Thr	Arg	Ala	Ala	Ser	Ile	Leu	Ser	Asp	Gly	Asp	Ile	Gly	Val	Asp	195	200	205
Ile	Ser	Leu	Thr	Gly	Asp	Pro	Val	Ile	Thr	Ala	Ser	Tyr	Leu	Glu	Ser	210	215	220
His	His	Lys	Gly	His	Phe	Ile	Tyr	Lys	Asn	Val	Ser	Glu	Asp	Leu	Pro	225	230	235
Leu	Pro	Thr	Phe	Ser	Pro	Thr	Leu	Leu	Gly	Asp	Ser	Arg	Met	Leu	Tyr	245	250	255
Phe	Trp	Phe	Ser	Glu	Arg	Val	Phe	His	Ser	Leu	Ala	Lys	Val	Ala	Phe	260	265	270
Gln	Asp	Gly	Arg	Leu	Met	Leu	Ser	Leu	Met	Gly	Asp	Glu	Phe	Lys	Ala	275	280	285
Val	Leu	Glu	Thr	Trp	Gly	Phe	Asn	Thr	Asn	Gln	Glu	Ile	Phe	Gln	Glu	290	295	300
Val	Val	Gly	Gly	Phe	Pro	Ser	Gln	Ala	Gln	Val	Thr	Val	His	Cys	Leu	305	310	315
Lys	Met	Pro	Lys	Ile	Ser	Cys	Gln	Asn	Lys	Gly	Val	Val	Val	Asn	Ser	325	330	335
Ser	Val	Met	Val	Lys	Phe	Leu	Phe	Pro	Arg	Pro	Asp	Gln	Gln	His	Ser	340	345	350
Val	Ala	Tyr	Thr	Phe	Glu	Glu	Asp	Ile	Val	Thr	Thr	Val	Gln	Ala	Ser	355	360	365
Tyr	Ser	Lys	Lys	Lys	Leu	Phe	Leu	Ser	Leu	Leu	Asp	Phe	Gln	Ile	Thr	370	375	380
Pro	Lys	Thr	Val	Ser	Asn	Leu	Thr	Glu	Ser	Ser	Ser	Glu	Ser	Ile	Gln	385	390	395
Ser	Phe	Leu	Gln	Ser	Met	Ile	Thr	Ala	Val	Gly	Ile	Pro	Glu	Val	Met	405	410	415
Ser	Arg	Leu	Glu	Val	Val	Phe	Thr	Ala	Leu	Met	Asn	Ser	Lys	Gly	Val	420	425	430

Ser Leu Phe Asp Ile Ile Asn Pro Glu Ile Ile Thr Arg Asp Gly Phe
435 440 445

Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu Val Asp
450 455 460

Phe Leu Gln Ser Leu Ser
465 470

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<211> 42
<212> DNA
<213> Human

<220>
<223> oligonucleotide from XcmI site to SphI site within
BPI gene (encoding residues 348-361) containing
the codon TCC for the serine at amino acid
position 351

<400> 7
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<210> 8
<211> 42
<212> DNA
<213> Human

<220>
<223> Oligonucleotide complementary to SEQ ID NO:5

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<210> 9
<211> 14
<212> PRT
<213> Human

<220>
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348-361 in BPI

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1 5 10

<210> 10
<211> 42
<212> DNA
<213> Human

<220>
<223> oligonucleotide from XcmI site to SphI site within
the BPI gene (encoding residues 348-361)
containing the codon GCC for alanine at amino acid
position 351

<400> 10
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42

<210> 11
<211> 42
<212> DNA
<213> Human

<220>
<223> Oligonucleotide complementary to SEQ ID NO:8

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42

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<211> 14
<212> PRT
<213> Human

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1 5 10